

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Artavanis-Tsakonas, S. et al.
- (ii) TITLE OF INVENTION: Therapeutic And Diagnostic Methods
And Compositions Based On Notch Proteins And
Nucleic Acids
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: Concurrently Herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Misrock, S. Leslie
 - (B) REGISTRATION NUMBER: 18,872
 - (C) REFERENCE/DOCKET NUMBER: 7326-015
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212 790-9090
 - (B) TELEFAX: 212 8698864/9741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2892 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 142..2640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA	60
CACACACACA CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA	120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA	171

ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly 270 275 280	987
TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His 285 290 295	1035
AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC GGC GAG GGA TTG Arg Pro Cys Lys Asn Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu 300 305 310	1083
TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn 315 320 325 330	1131
GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly 335 340 345	1179
ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys 350 355 360	1227
GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys 365 370 375	1275
TCG GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly 380 385 390	1323
TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr 395 400 405 410	1371
AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro 415 420 425	1419
TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA Cys Ile Asn Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro 430 435 440	1467
GCG GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu 445 450 455	1515
GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln 460 465 470	1563
TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser 475 480 485 490	1611
AAA GTT GAC TTG TGC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TGC Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys 495 500 505	1659
TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr 510 515 520	1707
GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys 525 530 535	1755

CAT His 540	AAC Asn	GGC Gly	GGC Gly	ACT Thr	TGC Cys	ATG Met	AAC Asn	CGC Arg	GTC Val	AAT Asn	TCG Ser	TTC Phe	GAA Glu	TGC Cys	GTG Val	1803
TGT Cys 555	GCC Ala	AAT Asn	GGT Gly	TTC Phe	AGG Arg	GGC Gly	AAG Lys	CAG Gln	TGC Cys	GAT Asp	GAG Glu	GAG Glu	TCC Ser	TAC Tyr	GAT Asp	1851
TCG Ser	GTG Val	ACC Thr	TTC Phe	GAT Asp	GCC Ala	CAC His	CAA Gln	TAT Tyr	GGA Gly	GCG Ala	ACC Thr	ACA Thr	CAA Gln	GCG Ala	AGA Arg	1899
GCC Ala	GAT Asp	GGT Gly	TTG Leu	ACC Thr	AAT Asn	GCC Ala	CAG Gln	GTA Val	GTC Val	CTA Leu	ATT Ile	GCT Ala	GTT Val	TTC Phe	TCC Ser	1947
GTT Val	GCG Ala	ATG Met	CCT Pro	TTG Leu	GTG Val	GCG Ala	GTT Val	ATT Ile	GCG Ala	GCG Ala	TGC Cys	GTG Val	GTC Val	TTC Phe	TGC Cys	1995
ATG Met	AAG Lys	CGC Arg	AAG Lys	CGT Arg	AAG Lys	CGT Arg	GCT Ala	CAG Gln	GAA Glu	AAG Lys	GAC Asp	GAC Asp	GCG Ala	GAG Glu	GCC Ala	2043
AGG Arg	AAG Lys	CAG Gln	AAC Asn	GAA Glu	CAG Gln	AAT Asn	GCG Ala	GTG Val	GCC Ala	ACA Thr	ATG Met	CAT His	CAC His	AAT Asn	GGC Gly	2091
AGT Ser	GGG Gly	GTG Val	GGT Gly	GTA Val	GCT Ala	TTG Leu	GCT Ala	TCA Ser	GCC Ala	TCT Ser	CTG Leu	GGC Gly	GGC Gly	AAA Lys	ACT Thr	2139
GGC Gly	AGC Ser	AAC Asn	AGC Ser	GGT Gly	CTC Leu	ACC Thr	TTC Phe	GAT Asp	GGC Gly	GGC Gly	AAC Asn	CCG Pro	AAT Asn	ATC Ile	ATC Ile	2187
AAA Lys	AAC Asn	ACC Thr	TGG Trp	GAC Asp	AAG Lys	TCG Ser	GTC Val	AAC Asn	AAC Asn	ATT Ile	TGT Cys	GCC Ala	TCA Ser	GCA Ala	GCA Ala	2235
GCA Ala	GCG Ala	GCG Ala	GCG Ala	GCG Ala	GCA Ala	GCA Ala	GCG Ala	GCG Ala	GAC Asp	GAG Glu	TGT Cys	CTC Leu	ATG Met	TAC Tyr	GGC Gly	2283
GGA Gly	TAT Tyr	GTG Val	GCC Ala	TCG Ser	GTG Val	GCG Ala	GAT Asp	AAC Asn	AAC Asn	AAT Asn	GCC Ala	AAC Asn	TCA Ser	GAC Asp	TTT Phe	2331
TGT Cys	GTG Val	GCT Ala	CCG Pro	CTA Leu	CAA Gln	AGA Arg	GCC Ala	AAG Lys	TCG Ser	CAA Gln	AAG Lys	CAA Gln	CTC Leu	AAC Asn	ACC Thr	2379
GAT Asp	CCC Pro	ACG Thr	CTC Leu	ATG Met	CAC His	CGC Arg	GGT Gly	TCG Ser	CCG Pro	GCA Ala	GGC Gly	AGC Ser	TCA Ser	GCC Ala	AAG Lys	2427
GGA Gly	GCG Ala	TCT Ser	GGC Gly	GGA Gly	GGA Gly	CCG Pro	GGA Gly	GCG Ala	GCG Ala	GAG Glu	GGC Gly	AAG Lys	AGG Arg	ATC Ile	TCT Ser	2475
GTT Val	TTA Leu	GGC Gly	GAG Glu	GGT Gly	TCC Ser	TAC Tyr	TGT Cys	AGC Ser	CAG Gln	CGT Arg	TGG Trp	CCC Pro	TCG Ser	TTG Leu	GCG Ala	2523
GCG Ala	GCG Ala	GGA Gly	GTG Val	GCC Ala	GGA Gly	GCC Ala	TGT Cys	TCA Ser	TCC Ser	CAG Gln	CTA Leu	ATG Met	GCT Ala	GCA Ala	GCT Ala	2571

TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG	2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val	
815 820 825	
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT	2670
Val Cys Gly Thr Pro His Met	
830	
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT	2730
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTGTG ATTGAAGCAG TTTAGTCGTC	2790
ACGAAAAATG AAAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
		20						25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35					40					45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
	50					55					60				
Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65				70				75							80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
			85					90						95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
		100						105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
	130					135					140				
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155					160
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
			165						170					175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
		180						185					190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			

Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp
 210 215 220
 Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys
 225 230 235 240
 Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu
 245 250 255
 Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn
 260 265 270
 Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys
 275 280 285
 Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly
 290 295 300
 Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu Tyr Thr Cys Lys Cys Ala
 305 310 315 320
 Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn Glu Ile Tyr Ser Cys Asp
 325 330 335
 Ala Asp Val Asn Pro Cys Gln Asn Gly Gly Thr Cys Ile Asp Glu Pro
 340 345 350
 His Thr Lys Thr Gly Tyr Lys Cys His Cys Ala Asn Gly Trp Ser Gly
 355 360 365
 Lys Met Cys Glu Glu Lys Val Leu Thr Cys Ser Asp Lys Pro Cys His
 370 375 380
 Gln Gly Ile Cys Arg Asn Val Arg Pro Gly Leu Gly Ser Lys Gly Gln
 385 390 395 400
 Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr Ser Gly Pro Asn Cys Asp
 405 410 415
 Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro Cys Ile Asn Gly Gly Ser
 420 425 430
 Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro Ala Gly Phe Ser Gly Thr
 435 440 445
 Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly His Gln Cys Glu Asn
 450 455 460
 Gly Gly Thr Cys Ile Asp Met Val Asn Gln Tyr Arg Cys Gln Cys Val
 465 470 475 480
 Pro Gly Phe His Gly Thr His Cys Ser Ser Lys Val Asp Leu Cys Leu
 485 490 495
 Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys Leu Asn Leu Asn Asn Asp
 500 505 510
 Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr Gly Lys Asp Cys Ser Val
 515 520 525
 Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys His Asn Gly Gly Thr Cys
 530 535 540
 Met Asn Arg Val Asn Ser Phe Glu Cys Val Cys Ala Asn Gly Phe Arg
 545 550 555 560
 Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp Ser Val Thr Phe Asp Ala

(B) LOCATION: 442..1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCCTT TTCTGTCAAC GCTAAAGATC	60
TACAAAACAT CAGCGCCTAT CAAGTGAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
CCAAATCTG CATACATGGG CTAATTAAGG CTGCCCAGCG AATTACATT TGTGTGGTGC	360
CAATCCAGAG TGAATCCGAA ACAAACTCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA	471
Met Phe Arg Lys His Phe Arg Arg Lys Pro	
1 5 10	
GCT ACG TCG TCG TCG TTG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG	519
Ala Thr Ser Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu	
15 20 25	
GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG	567
Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg	
30 35 40	
GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA	615
Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser	
45 50 55	
TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC	663
Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Leu Val	
60 65 70	
CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711
His Lys Ile Ser Ala Ala Gly Asn Phe Glu Leu Glu Ile Leu Glu Ile	
75 80 85 90	
TCA AAT ACC AAC AGC CAT CTA CTC AAC GGC TAT TGC TGC GGC ATG CCA	759
Ser Asn Thr Asn Ser His Leu Leu Asn Gly Tyr Cys Cys Gly Met Pro	
95 100 105	
GCG GAA CTT AGG GCC ACC AAG ACG ATA GGC TGC TCG CCA TGC ACG ACG	807
Ala Glu Leu Arg Ala Thr Lys Thr Ile Gly Cys Ser Pro Cys Thr Thr	
110 115 120	
GCA TTC CGG CTG TGC CTG AAG GAG TAC CAG ACC ACG GAG CAG GGT GCC	855
Ala Phe Arg Leu Cys Leu Lys Glu Tyr Gln Thr Thr Glu Gln Gly Ala	
125 130 135	
AGC ATA TCC ACG GGC TGT TCG TTT GGC AAC GCC ACC ACC AAG ATA CTG	903
Ser Ile Ser Thr Gly Cys Ser Phe Gly Asn Ala Thr Thr Lys Ile Leu	
140 145 150	
GGT GGC TCC AGC TTT GTG CTC AGC GAT CCG GGT GTG GGA GCC ATT GTG	951
Gly Gly Ser Ser Phe Val Leu Ser Asp Pro Gly Val Gly Ala Ile Val	
155 160 165 170	
CTG CCC TTT ACG TTT CGT TGG ACG AAG TCG TTT ACG CTG ATA CTG CAG	999
Leu Pro Phe Thr Phe Arg Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln	
175 180 185	
GCG TTG GAT ATG TAC AAC ACA TCC TAT CCA GAT GCG GAG AGG TTA ATT	1047

Ala	Leu	Asp	Met	Tyr	Asn	Thr	Ser	Tyr	Pro	Asp	Ala	Glu	Arg	Leu	Ile		
			190					195					200				
GAG	GAA	ACA	TCA	TAC	TCG	GGC	GTG	ATA	CTG	CCG	TCG	CCG	GAG	TGG	AAG	1095	
Glu	Glu	Thr	Ser	Tyr	Ser	Gly	Val	Ile	Leu	Pro	Ser	Pro	Glu	Trp	Lys		
			205				210					215					
ACG	CTG	GAC	CAC	ATC	GGG	CGG	AAC	GCG	CGG	ATC	ACC	TAC	CGT	GTC	CGG	1143	
Thr	Leu	Asp	His	Ile	Gly	Arg	Asn	Ala	Arg	Ile	Thr	Tyr	Arg	Val	Arg		
			220				225					230					
GTG	CAA	TGC	GCC	GTT	ACC	TAC	TAC	AAC	ACG	ACC	TGC	ACG	ACC	TTC	TGC	1191	
Val	Gln	Cys	Ala	Val	Thr	Tyr	Tyr	Asn	Thr	Thr	Cys	Thr	Thr	Phe	Cys		
					240					245					250		
CGT	CCG	CGG	GAC	GAT	CAG	TTC	GGT	CAC	TAC	GCC	TGC	GGC	TCC	GAG	GGT	1239	
Arg	Pro	Arg	Asp	Asp	Gln	Phe	Gly	His	Tyr	Ala	Cys	Gly	Ser	Glu	Gly		
				255					260					265			
CAG	AAG	CTC	TGC	CTG	AAT	GGC	TGG	CAG	GGC	GTC	AAC	TGC	GAG	GAG	GCC	1287	
Gln	Lys	Leu	Cys	Leu	Asn	Gly	Trp	Gln	Gly	Val	Asn	Cys	Glu	Glu	Ala		
			270					275					280				
ATA	TGC	AAG	GCG	GGC	TGC	GAC	CCC	GTC	CAC	GGC						1320	
Ile	Cys	Lys	Ala	Gly	Cys	Asp	Pro	Val	His	Gly							
			285				290										

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Arg	Lys	His	Phe	Arg	Arg	Lys	Pro	Ala	Thr	Ser	Ser	Ser	Leu		
1				5					10						15		
Glu	Ser	Thr	Ile	Glu	Ser	Ala	Asp	Ser	Leu	Gly	Met	Ser	Lys	Lys	Thr		
			20					25					30				
Ala	Thr	Lys	Arg	Gln	Arg	Pro	Arg	His	Arg	Val	Pro	Lys	Ile	Ala	Thr		
			35			40						45					
Leu	Pro	Ser	Thr	Ile	Arg	Asp	Cys	Arg	Ser	Leu	Lys	Ser	Ala	Cys	Asn		
	50					55					60						
Leu	Ile	Ala	Leu	Ile	Leu	Ile	Leu	Val	His	Lys	Ile	Ser	Ala	Ala			
65				70				75						80			
Gly	Asn	Phe	Glu	Leu	Glu	Ile	Leu	Glu	Ile	Ser	Asn	Thr	Asn	Ser	His		
			85					90					95				
Leu	Leu	Asn	Gly	Tyr	Cys	Cys	Gly	Met	Pro	Ala	Glu	Leu	Arg	Ala	Thr		
			100					105					110				
Lys	Thr	Ile	Gly	Cys	Ser	Pro	Cys	Thr	Thr	Ala	Phe	Arg	Leu	Cys	Leu		
		115					120					125					
Lys	Glu	Tyr	Gln	Thr	Thr	Glu	Gln	Gly	Ala	Ser	Ile	Ser	Thr	Gly	Cys		
	130					135					140						
Ser	Phe	Gly	Asn	Ala	Thr	Thr	Lys	Ile	Leu	Gly	Gly	Ser	Ser	Phe	Val		

145		150		155		160
Leu Ser Asp Pro Gly Val Gly Ala Ile Val Leu Pro Phe Thr Phe Arg						
	165			170		175
Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln Ala Leu Asp Met Tyr Asn						
	180		185		190	
Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile Glu Glu Thr Ser Tyr Ser						
	195		200		205	
Gly Val Ile Leu Pro Ser Pro Glu Trp Lys Thr Leu Asp His Ile Gly						
	210		215		220	
Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg Val Gln Cys Ala Val Thr						
	225		230		235	240
Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys Arg Pro Arg Asp Asp Gln						
		245		250		255
Phe Gly His Tyr Ala Cys Gly Ser Glu Gly Gln Lys Leu Cys Leu Asn						
		260		265		270
Gly Trp Gln Gly Val Asn Cys Glu Glu Ala Ile Cys Lys Ala Gly Cys						
	275		280		285	
Asp Pro Val His Gly						
	290					

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTGGACTT CCTTCGTGTA TTGGTGGGAG CCCTCGGGAA CGGGGGGTAA CACTGAAAGG	60
TCGAGTACCC ATTTCCGTCA TAACGGGTTG GTCGCCCCCT AGGGGTCGGA GTCAGGTGGA	120
CGGGAGGTCG ACAACGCCCG GGGGACGGGT GGTACATGGT GTAAGGTCTT TACCGGACCG	180
GGCAAACGGG TCACACCGAA AGGGGTGAAC GGTAAC TACG GGGTCGTCCT GCCCGTCCAT	240
CGAGTCTGGT AAGAGGGTCG CCTTAAG	267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCTTC CATTATACGT GACTTTTCTG AAAGTGTAGC CACCCTAGTG TCTCTAACTC	60
CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT	120
GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
AACCCGGAAC TGAAGGCTGG CTCTCACCCCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
TGTTAGATGT GAATGTCCGT GGCCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC	300
GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA	360
TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGAAGTGGTA	420
GATGGCCCTG CACCTTGACG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT	540
GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA	574

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCAGATTCT GATTGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180
CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTTGAAAAA TGGGGCCAAC CGAGACATGC	240
AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCG GGAGGAGCTA TAAGC	295

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG	60
ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA	120
TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180

GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG 240
CAGAGCTG 248

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTTNNNA GTGCGAGGGA CATTCGTCCG 60
ACCA GTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG 120
GAGCTACAGG TCCC GCTCGC TAAACTCGGA CCACTGAAAC CTCCGGTCGA CAGTCGGTAA 180
GCGAACAAGA GGGCCAGATC TTAGAGAAGG TGTCGCGGCG AGACTCGGGC TCGGGTCAGG 240
CGGCCTTAAG GACGTCGGGC CCNNNAGGTG ATCAAGATCT CGNCNCGGCG GCGGCCACCT 300
CGAGGNCGAA AACAAGGGAA ATC 323

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..3234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC 48
Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn
1 5 10 15
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 96
His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp
20 25 30
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT 144
Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser
35 40 45
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 192
Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp
50 55 60
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 240

Gly 65	Phe	Asp	Cys	Gln	Arg 70	Ala	Glu	Gly	Gln	Cys 75	Asn	Pro	Leu	Tyr	Asp 80	
CAG Gln	TAC Tyr	TGC Cys	AAG Lys	GAC Asp 85	CAC His	TTC Phe	AGC Ser	GAC Asp	GGG Gly 90	CAC His	TGC Cys	GAC Asp	CAG Gln	GGC Gly 95	TGC Cys	288
AAC Asn	AGC Ser	GCG Ala	GAG Glu 100	TGC Cys	GAG Glu	TGG Trp	GAC Asp	GGG Gly 105	CTG Leu	GAC Asp	TGT Cys	GCG Ala	GAG Glu 110	CAT His	GTA Val	336
CCC Pro	GAG Glu	AGG Arg 115	CTG Leu	GCG Ala	GCC Ala	GGC Gly	ACG Thr 120	CTG Leu	GTG Val	GTG Val	GTG Val	GTG Val	CTG Leu	ATG Met	CCG Pro	384
CCG Pro	GAG Glu	CAG Gln 130	CTG Leu	GCG Arg	AAC Asn	AGC Ser 135	TCC Ser	TTC Phe	CAC His	TTC Phe	CTG Leu	CGG Arg	GAG Glu	CTC Leu	AGC Ser	432
CGC Arg 145	GTG Val	CTG Leu	CAC His	ACC Thr	AAC Asn 150	GTG Val	GTC Val	TTC Phe	AAG Lys 155	CGT Arg	GAC Asp	GCA Ala	CAC His	GGC Gly	CAG Gln 160	480
CAG Gln	ATG Met	ATC Ile	TTC Phe	CCC Pro 165	TAC Tyr	TAC Tyr	GGC Gly	CGC Arg	GAG Glu 170	GAG Glu	GAG Glu	CTG Leu	CGC Arg	AAG Lys 175	CAC His	528
CCC Pro	ATC Ile	AAG Lys 180	CGT Arg	GCC Ala	GCC Ala	GAG Glu	GGC Gly	TGG Trp 185	GCC Ala	GCA Ala	CCT Pro	GAC Asp	GCC Ala 190	CTG Leu	CTG Leu	576
GGC Gly	CAG Gln	GTG Val 195	AAG Lys	GCC Ala	TCG Ser	CTG Leu	CTC Leu 200	CCT Pro	GGT Gly	GGC Gly	AGC Ser	GAG Glu 205	GGT Gly	GGG Gly	CGG Arg	624
CGG Arg 210	CGG Arg	AGG Arg	GAG Glu	CTG Leu	GAC Asp 215	CCC Pro	ATG Met	GAC Asp	GTC Val	CGC Arg	GGC Gly 220	TCC Ser	ATC Ile	GTC Val	TAC Tyr	672
CTG Leu 225	GAG Glu	ATT Ile	GAC Asp	AAC Asn 230	CGG Arg	CAG Gln	TGT Cys	GTG Val	CAG Gln	GCC Ala 235	TCC Ser	TCG Ser	CAG Gln	TGC Cys	TTC Phe 240	720
CAG Gln	AGT Ser	GCC Ala	ACC Thr	GAC Asp 245	GTG Val	GCC Ala	GCA Ala	TTC Phe	CTG Leu 250	GGA Gly	GCG Ala	CTC Leu	GCC Ala	TCG Ser	CTG Leu 255	768
GGC Gly	AGC Ser	CTC Leu	AAC Asn 260	ATC Ile	CCC Pro	TAC Tyr	AAG Lys	ATC Ile 265	GAG Glu	GCC Ala	GTG Val	CAG Gln	AGT Ser 270	GAG Glu	ACC Thr	816
GTG Val	GAG Glu	CCG Pro 275	CCC Pro	CCG Pro	GCG Ala	CAG Gln 280	CTG Leu	CAC His	TTC Phe	ATG Met	TAC Tyr 285	GTG Val	GCG Ala	GCG Ala		864
GCC Ala 290	GCC Ala	TTT Phe	GTG Val	CTT Leu	CTG Leu	TTC Phe 295	TTC Phe	GTG Val	GGC Gly	TGC Cys	GGG Gly 300	GTG Val	CTG Leu	CTG Leu	TCC Ser	912
CGC Arg 305	AAG Lys	CGC Arg	CGG Arg	CGG Arg	CAG Gln 310	CAT His	GGC Gly	CAG Gln	CTC Leu	TGG Trp 315	TTC Phe	CCT Pro	GAG Glu	GGC Gly	TTC Phe 320	960
AAA Lys	GTG Val	TCT Ser	GAG Glu	GCC Ala 325	AGC Ser	AAG Lys	AAG Lys	AAG Lys	CGG Arg 330	CGG Arg	GAG Glu	CCC Pro	CTC Leu	GGC Gly 335	GAG Glu	1008

GAC	TCC	GTG	GGC	CTC	AAG	CCC	CTG	AAG	AAC	GCT	TCA	GAC	GGT	GCC	CTC	1056
Asp	Ser	Val	Gly	Leu	Lys	Pro	Leu	Lys	Asn	Ala	Ser	Asp	Gly	Ala	Leu	
			340					345					350			
ATG	GAC	GAC	AAC	CAG	AAT	GAG	TGG	GGG	GAC	GAG	GAC	CTG	GAG	ACC	AAG	1104
Met	Asp	Asp	Asn	Gln	Asn	Glu	Trp	Gly	Asp	Glu	Asp	Leu	Glu	Thr	Lys	
			355				360					365				
AAG	TTC	CGG	TTC	GAG	GAG	CCC	GTG	GTT	CTG	CCT	GAC	CTG	GAC	GAC	CAG	1152
Lys	Phe	Arg	Phe	Glu	Glu	Pro	Val	Val	Leu	Pro	Asp	Leu	Asp	Asp	Gln	
	370					375					380					
ACA	GAC	CAC	CGG	CAG	TGG	ACT	CAG	CAG	CAC	CTG	GAT	GCC	GCT	GAC	CTG	1200
Thr	Asp	His	Arg	Gln	Trp	Thr	Gln	Gln	His	Leu	Asp	Ala	Ala	Asp	Leu	
385					390					395					400	
CGC	ATG	TCT	GCC	ATG	GCC	CCC	ACA	CCG	CCC	CAG	GGT	GAG	GTT	GAC	GCC	1248
Arg	Met	Ser	Ala	Met	Ala	Pro	Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala	
				405					410					415		
GAC	TGC	ATG	GAC	GTC	AAT	GTC	CGC	GGG	CCT	GAT	GGC	TTC	ACC	CCG	CTC	1296
Asp	Cys	Met	Asp	Val	Asn	Val	Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu	
			420					425					430			
ATG	ATC	GCC	TCC	TGC	AGC	GGG	GGC	GGC	CTG	GAG	ACG	GGC	AAC	AGC	GAG	1344
Met	Ile	Ala	Ser	Cys	Ser	Gly	Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	
		435					440					445				
GAA	GAG	GAG	GAC	GCG	CCG	GCC	GTC	ATC	TCC	GAC	TTC	ATC	TAC	CAG	GGC	1392
Glu	Glu	Glu	Asp	Ala	Pro	Ala	Val	Ile	Ser	Asp	Phe	Ile	Tyr	Gln	Gly	
	450					455					460					
GCC	AGC	CTG	CAC	AAC	CAG	ACA	GAC	CGC	ACG	GGC	GAG	ACC	GCC	TTG	CAC	1440
Ala	Ser	Leu	His	Asn	Gln	Thr	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	
465					470					475					480	
CTG	GCC	GCC	CGC	TAC	TCA	CGC	TCT	GAT	GCC	GCC	AAG	CGC	CTG	CTG	GAG	1488
Leu	Ala	Ala	Arg	Tyr	Ser	Arg	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu	
				485				490						495		
GCC	AGC	GCA	GAT	GCC	AAC	ATC	CAG	GAC	AAC	ATG	GGC	CGC	ACC	CCG	CTG	1536
Ala	Ser	Ala	Asp	Ala	Asn	Ile	Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu	
			500					505					510			
CAT	GCG	GCT	GTG	TCT	GCC	GAC	GCA	CAA	GGT	GTC	TTC	CAG	ATC	CTG	ATC	1584
His	Ala	Ala	Val	Ser	Ala	Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile	
		515					520					525				
CGG	AAC	CGA	GCC	ACA	GAC	CTG	GAT	GCC	CGC	ATG	CAT	GAT	GGC	ACG	ACG	1632
Arg	Asn	Arg	Ala	Thr	Asp	Leu	Asp	Ala	Arg	Met	His	Asp	Gly	Thr	Thr	
	530					535					540					
CCA	CTG	ATC	CTG	GCT	GCC	CGC	CTG	GCC	GTG	GAG	GGC	ATG	CTG	GAG	GAC	1680
Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	Gly	Met	Leu	Glu	Asp	
545					550					555					560	
CTC	ATC	AAC	TCA	CAC	GCC	GAC	GTC	AAC	GCC	GTA	GAT	GAC	CTG	GGC	AAG	1728
Leu	Ile	Asn	Ser	His	Ala	Asp	Val	Asn	Ala	Val	Asp	Asp	Leu	Gly	Lys	
				565				570						575		
TCC	GCC	CTG	CAC	TGG	GCC	GCC	GCC	GTG	AAC	AAT	GTG	GAT	GCC	GCA	GTT	1776
Ser	Ala	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val	
			580					585					590			
GTG	CTC	CTG	AAG	AAC	GGG	GCT	AAC	AAA	GAT	ATG	CAG	AAC	AAC	AGG	GAG	1824
Val	Leu	Leu	Lys	Asn	Gly	Ala	Asn	Lys	Asp	Met	Gln	Asn	Asn	Arg	Glu	
		595					600					605				

GAG Glu 610	ACA Thr 610	CCC Pro 610	CTG Leu 610	TTT Phe 610	CTG Leu 615	GCC Ala 615	GCC Ala 615	CGG Arg 615	GAG Glu 620	GGC Gly 620	AGC Ser 620	TAC Tyr 620	GAG Glu 620	ACC Thr 620	GCC Ala 620	1872
AAG Lys 625	GTG Val 625	CTG Leu 625	CTG Leu 625	GAC Asp 630	CAC His 630	TTT Phe 630	GCC Ala 630	AAC Asn 630	CGG Arg 635	GAC Asp 635	ATC Ile 635	ACG Thr 635	GAT Asp 640	CAT His 640	ATG Met 640	1920
GAC Asp 645	CGC Arg 645	CTG Leu 645	CCG Pro 645	CGC Arg 645	GAC Asp 645	ATC Ile 645	GCA Ala 645	CAG Gln 645	GAG Glu 650	CGC Arg 650	ATG Met 650	CAT His 655	CAC His 655	GAC Asp 655	ATC Ile 655	1968
GTG Val 660	AGG Arg 660	CTG Leu 660	CTG Leu 660	GAC Asp 660	GAG Glu 660	TAC Tyr 660	AAC Asn 665	CTG Leu 665	GTG Val 665	CGC Arg 665	AGC Ser 665	CCG Pro 665	CAG Gln 670	CTG Leu 670	CAC His 670	2016
GGA Gly 675	GCC Ala 675	CCG Pro 675	CTG Leu 675	GGG Gly 675	GGC Gly 675	ACG Thr 675	CCC Pro 680	ACC Thr 680	CTG Leu 680	TCG Ser 680	CCC Pro 685	CCG Pro 685	CTC Leu 685	TGC Cys 685	TCG Ser 685	2064
CCC Pro 690	AAC Asn 690	GGC Gly 690	TAC Tyr 690	CTG Leu 690	GGC Gly 695	AGC Ser 695	CTC Leu 695	AAG Lys 695	CCC Pro 700	GGC Gly 700	GTG Val 700	CAG Gln 700	GGC Gly 700	AAG Lys 700	AAG Lys 700	2112
GTC Val 705	CGC Arg 705	AAG Lys 705	CCC Pro 705	AGC Ser 710	AGC Ser 710	AAA Lys 710	GGC Gly 710	CTG Leu 710	GCC Ala 715	TGT Cys 715	GGA Gly 715	AGC Ser 715	AAG Lys 715	GAG Glu 720	GCC Ala 720	2160
AAG Lys 725	GAC Asp 725	CTC Leu 725	AAG Lys 725	GCA Ala 725	CGG Arg 725	AGG Arg 725	AAG Lys 725	AAG Lys 725	TCC Ser 730	CAG Gln 730	GAT Asp 730	GGC Gly 735	AAG Lys 735	GGC Gly 735	TGC Cys 735	2208
CTG Leu 740	CTG Leu 740	GAC Asp 740	AGC Ser 740	TCC Ser 740	GGC Gly 740	ATG Met 745	CTC Leu 745	TCG Ser 745	CCC Pro 745	GTG Val 745	GAC Asp 745	TCC Ser 750	CTG Leu 750	GAG Glu 750	TCA Ser 750	2256
CCC Pro 755	CAT His 755	GGC Gly 755	TAC Tyr 755	CTG Leu 755	TCA Ser 760	GAC Asp 760	GTG Val 760	GCC Ala 760	TCG Ser 760	CCG Pro 765	CCA Pro 765	CTG Leu 765	CTG Leu 765	CCC Pro 765	TCC Ser 765	2304
CCG Pro 770	TTC Phe 770	CAG Gln 770	CAG Gln 770	TCT Ser 775	CCG Pro 775	TCC Ser 775	GTG Val 775	CCC Pro 775	CTC Leu 780	AAC Asn 780	CAC His 780	CTG Leu 780	CCT Pro 780	GGG Gly 780	ATG Met 780	2352
CCC Pro 785	GAC Asp 785	ACC Thr 785	CAC His 785	CTG Leu 790	GGC Gly 790	ATC Ile 790	GGG Gly 790	CAC His 795	CTG Leu 795	AAC Asn 795	GTG Val 795	GCG Ala 795	GCC Ala 795	AAG Lys 800	CCC Pro 800	2400
GAG Glu 805	ATG Met 805	GCG Ala 805	GCG Ala 805	CTG Leu 805	GGT Gly 805	GGG Gly 805	GGC Gly 805	CGG Arg 810	CTG Leu 810	GCC Ala 810	TTT Phe 815	GAG Glu 815	ACT Thr 815	GGC Gly 815		2448
CCA Pro 820	CCT Pro 820	CGT Arg 820	CTC Leu 820	TCC Ser 820	CAC His 820	CTG Leu 825	CCT Pro 825	GTG Val 825	GCC Ala 825	TCT Ser 825	GGC Gly 830	ACC Thr 830	AGC Ser 830	ACC Thr 830	GTC Val 830	2496
CTG Leu 835	GGC Gly 835	TCC Ser 835	AGC Ser 835	AGC Ser 835	GGA Gly 840	GGG Gly 840	GCC Ala 840	CTG Leu 840	AAT Asn 845	TTC Phe 845	ACT Thr 845	GTG Val 845	GGC Gly 845	GGG Gly 845	TCC Ser 845	2544
ACC Thr 850	AGT Ser 850	TTG Leu 850	AAT Asn 850	GGT Gly 855	CAA Gln 855	TGC Cys 855	GAG Glu 855	TGG Trp 855	CTG Leu 860	TCC Ser 860	CGG Arg 860	CTG Leu 860	CAG Gln 860	AGC Ser 860	GGC Gly 860	2592
ATG Met 865	GTG Val 865	CCG Pro 865	AAC Asn 865	CAA Gln 870	TAC Tyr 870	AAC Asn 870	CCT Pro 870	CTG Leu 870	CGG Arg 875	GGG Gly 875	AGT Ser 875	GTG Val 875	GCA Ala 875	CCA Pro 880	GGC Gly 880	2640

CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG Pro Leu Ser Thr 885 Gln Ala Pro Ser Leu 890 Gln His Gly Met Val Gly Pro 895	2688
CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC Leu His Ser 900 Leu Ala Ala Ser 905 Leu Ser Gln Met Met Ser Tyr 910	2736
CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG Gln Gly Leu 915 Pro Ser Thr Arg Leu 920 Ala Thr Gln Pro His Leu Val Gln 925	2784
ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu 930 935 940	2832
CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA Gln Pro Ala Asn Ile 945 Gln Gln Gln Gln Ser Leu 955 Gln Pro Pro Pro Pro 960	2880
CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG Pro Pro Gln Pro His Leu Gly Val Ser 965 Ser Ala Ala Ser Gly His Leu 975	2928
GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA Gly Arg Ser 980 Phe Leu Ser Gly Glu 985 Pro Ser Gln Ala Asp Val Gln Pro 990	2976
CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC Leu Gly Pro 995 Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser 1000 1005	3024
CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC Pro Ala Leu 1010 Pro Thr Ser 1015 Leu Pro Ser Ser Leu Val Pro Pro Val Thr 1020	3072
GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro 1025 1030 1035 1040	3120
GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG Val Asp Asn Thr 1045 Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met 1050 1055	3168
GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile 1060 1065 1070	3216
GAA GCT CCC GAC TCA TGG Glu Ala Pro Asp Ser Trp 1075	3234

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn
1 5 10 15

His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp
 20 25 30
 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser
 35 40 45
 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp
 50 55 60
 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp
 65 70 75 80
 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys
 85 90 95
 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val
 100 105 110
 Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro
 115 120 125
 Pro Glu Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser
 130 135 140
 Arg Val Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln
 145 150 155 160
 Gln Met Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His
 165 170 175
 Pro Ile Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu
 180 185 190
 Gly Gln Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg
 195 200 205
 Arg Arg Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr
 210 215 220
 Leu Glu Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe
 225 230 235 240
 Gln Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu
 245 250 255
 Gly Ser Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr
 260 265 270
 Val Glu Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala
 275 280 285
 Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser
 290 295 300
 Arg Lys Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe
 305 310 315 320
 Lys Val Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Pro Leu Gly Glu
 325 330 335
 Asp Ser Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu
 340 345 350
 Met Asp Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys
 355 360 365
 Lys Phe Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln

370	375	380
Thr Asp His Arg Gln Trp	Thr Gln Gln His Leu	Asp Ala Ala Asp Leu
385	390	395 400
Arg Met Ser Ala Met Ala	Pro Thr Pro Pro Gln	Gly Glu Val Asp Ala
	405	410 415
Asp Cys Met Asp Val Asn	Val Arg Gly Pro Asp	Gly Phe Thr Pro Leu
	420	425 430
Met Ile Ala Ser Cys Ser	Gly Gly Gly Leu Glu	Thr Gly Asn Ser Glu
	435	440 445
Glu Glu Glu Asp Ala Pro	Ala Val Ile Ser Asp	Phe Ile Tyr Gln Gly
	450	455 460
Ala Ser Leu His Asn Gln	Thr Asp Arg Thr Gly	Glu Thr Ala Leu His
	465	470 475 480
Leu Ala Ala Arg Tyr Ser	Arg Ser Asp Ala Ala	Lys Arg Leu Leu Glu
	485	490 495
Ala Ser Ala Asp Ala Asn	Ile Gln Asp Asn Met	Gly Arg Thr Pro Leu
	500	505 510
His Ala Ala Val Ser Ala	Asp Ala Gln Gly Val	Phe Gln Ile Leu Ile
	515	520 525
Arg Asn Arg Ala Thr Asp	Leu Asp Ala Arg Met	His Asp Gly Thr Thr
	530	535 540
Pro Leu Ile Leu Ala Ala	Arg Leu Ala Val Glu	Gly Met Leu Glu Asp
	545	550 555 560
Leu Ile Asn Ser His Ala	Asp Val Asn Ala Val	Asp Asp Leu Gly Lys
	565	570 575
Ser Ala Leu His Trp Ala	Ala Ala Val Asn Asn	Val Asp Ala Ala Val
	580	585 590
Val Leu Leu Lys Asn Gly	Ala Asn Lys Asp Met	Gln Asn Asn Arg Glu
	595	600 605
Glu Thr Pro Leu Phe Leu	Ala Ala Arg Glu Gly	Ser Tyr Glu Thr Ala
	610	615 620
Lys Val Leu Leu Asp His	Phe Ala Asn Arg Asp	Ile Thr Asp His Met
	625	630 635 640
Asp Arg Leu Pro Arg Asp	Ile Ala Gln Glu Arg	Met His His Asp Ile
	645	650 655
Val Arg Leu Leu Asp Glu	Tyr Asn Leu Val Arg	Ser Pro Gln Leu His
	660	665 670
Gly Ala Pro Leu Gly Gly	Thr Pro Thr Leu Ser	Pro Pro Leu Cys Ser
	675	680 685
Pro Asn Gly Tyr Leu Gly	Ser Leu Lys Pro Gly	Val Gln Gly Lys Lys
	690	695 700
Val Arg Lys Pro Ser Ser	Lys Gly Leu Ala Cys	Gly Ser Lys Glu Ala
	705	710 715 720
Lys Asp Leu Lys Ala Arg	Arg Lys Lys Ser Gln	Asp Gly Lys Gly Cys
	725	730 735

Leu Leu Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser
 740 745 750
 Pro His Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser
 755 760 765
 Pro Phe Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met
 770 775 780
 Pro Asp Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro
 785 790 795 800
 Glu Met Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly
 805 810 815
 Pro Pro Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val
 820 825 830
 Leu Gly Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser
 835 840 845
 Thr Ser Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly
 850 855 860
 Met Val Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly
 865 870 875 880
 Pro Leu Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro
 885 890 895
 Leu His Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr
 900 905 910
 Gln Gly Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln
 915 920 925
 Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu
 930 935 940
 Gln Pro Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro
 945 950 955 960
 Pro Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu
 965 970 975
 Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro
 980 985 990
 Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser
 995 1000 1005
 Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr
 1010 1015 1020
 Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro
 1025 1030 1035 1040
 Val Asp Asn Thr Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met
 1045 1050 1055
 Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile
 1060 1065 1070
 Glu Ala Pro Asp Ser Trp
 1075

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..1972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys 1 5 10 15	46
ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser 20 25 30	94
GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp 35 40 45	142
TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly 50 55 60	190
GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala 65 70 75	238
AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met 80 85 90 95	286
GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val 100 105 110	334
TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met 115 120 125	382
AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu 130 135 140	430
GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val 145 150 155	478
GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn 160 165 170 175	526
GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met 180 185 190	574
CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly 195 200 205	622

AGC TAT GAA GCA GCC AAG ATC CTG TTA GAC CAT TTT GCC AAT CGA GAC Ser Tyr Glu Ala Ala Lys Ile Leu Asp His Phe Ala Asn Arg Asp 210 215 220	670
ATC ACA GAC CAT ATG GAT CGT CTT CCC CGG GAT GTG GCT CGG GAT CGC Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg 225 230 235	718
ATG CAC CAT GAC ATT GTG CGC CTT CTG GAT GAA TAC AAT GTG ACC CCA Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro 240 245 250 255	766
AGC CCT CCA GGC ACC GTG TTG ACT TCT GCT CTC TCA CCT GTC ATC TGT Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys 260 265 270	814
GGG CCC AAC AGA TCT TTC CTC AGC CTG AAG CAC ACC CCA ATG GGC AAG Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys 275 280 285	862
AAG TCT AGA CGG CCC AGT GCC AAG AGT ACC ATG CCT ACT AGC CTC CCT Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro 290 295 300	910
AAC CTT GCC AAG GAG GCA AAG GAT GCC AAG GGT AGT AGG AGG AAG AAG Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys 305 310 315	958
TCT CTG AGT GAG AAG GTC CAA CTG TCT GAG AGT TCA GTA ACT TTA TCC Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Val Thr Leu Ser 320 325 330 335	1006
CCT GTT GAT TCC CTA GAA TCT CCT CAC ACG TAT GTT TCC GAC ACC ACA Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr 340 345 350	1054
TCC TCT CCA ATG ATT ACA TCC CCT GGG ATC TTA CAG GCC TCA CCC AAC Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn 355 360 365	1102
CCT ATG TTG GCC ACT GCC GCC CCT CCT GCC CCA GTC CAT GCC CAG CAT Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His 370 375 380	1150
GCA CTA TCT TTT TCT AAC CTT CAT GAA ATG CAG CCT TTG GCA CAT GGG Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly 385 390 395	1198
GCC AGC ACT GTG CTT CCC TCA GTG AGC CAG TTG CTA TCC CAC CAC CAC Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His 400 405 410 415	1246
ATT GTG TCT CCA GGC AGT GGC AGT GCT GGA AGC TTG AGT AGG CTC CAT Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His 420 425 430	1294
CCA GTC CCA GTC CCA GCA GAT TGG ATG AAC CGC ATG GAG GTG AAT GAG Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu 435 440 445	1342
ACC CAG TAC AAT GAG ATG TTT GGT ATG GTC CTG GCT CCA GCT GAG GGC Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly 450 455 460	1390
ACC CAT CCT GGC ATA GCT CCC CAG AGC AGG CCA CCT GAA GGG AAG CAC Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His 465 470 475	1438

ATA ACC ACC CCT CGG GAG CCC TTG CCC CCC ATT GTG ACT TTC CAG CTC Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu 480 485 490 495	1486
ATC CCT AAA GGC AGT ATT GCC CAA CCA GCG GGG GCT CCC CAG CCT CAG Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln 500 505 510	1534
TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATG TAC CAG Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln 515 520 525	1582
ATT CCA GAA ATG GCC CGT TTG CCC AGT GTG GCT TTC CCC ACT GCC ATG Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met 530 535 540	1630
ATG CCC CAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr 545 550 555	1678
CAT CCT TTC CCA GCC TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln 560 565 570 575	1726
CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser 580 585 590	1774
GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser 595 600 605	1822
CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser 610 615 620	1870
GAT GTG ACC ACC AGC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CGG Asp Val Thr Thr Ser Pro Pro Gly Gly Ala Gly Gly Gly Gln Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAGA TGTTCTTATT CAGATAATGC AAGAGAAGCA ATTCGTCACT	2142
TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAATCT AATAAGACAA GTTTGTGGAA	2202
ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTTACTCTC TTCTATTTGG AGAATAAGAT	2262
GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCCCTG TTGGGAATTA TGCCCTGGAA	2382
TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTTGT CTTCATTTGG	2442
TGCTTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC	2502
CTTTGTGCTT TTGATCATTC TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCGGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC	2622

TTTCAAGTAT GTTGTTCCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT	2682
CATTCCTGGA GAGAGAAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG	2742
ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT	2802
TTACCAGGAA GAAGGGTGTG AGTTTGTGTG TTTTCTGTGT ATGGGCCTGG TCAGTGTAAG	2862
GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG	2922
GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT	3042
CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCCTCACC CAGCATATGA AACTAGTCTT	3102
AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG	3162
CCATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT	3222
CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT	3282
TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT	3342
TTATATGTTT AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC	3402
CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT	3462
TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG	3522
AACATTTTCC TTTCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA	3582
TTGTTGAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT	3642
TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTTAGTTAAT TGTAAGATAA GAATAGTTTT	3702
CTTCCTCTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC	3762
AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAAGATAT	3822
AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCTT CTATGGCTGC	3882
AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAC	3942
CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT	4002
TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC	4062
TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT	4122
TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG	4242
GCGATGGCGA TGACTTTCTT CCCCTG	4268

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr
 1 5 10 15
 Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser Asp
 20 25 30
 Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu
 35 40 45
 Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu
 50 55 60
 Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala Lys
 65 70 75 80
 Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly
 85 90 95
 Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe
 100 105 110
 Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn
 115 120 125
 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly
 130 135 140
 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp
 145 150 155 160
 Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Val Asn Asn Val
 165 170 175
 Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met Gln
 180 185 190
 Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser
 195 200 205
 Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp Ile
 210 215 220
 Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg Met
 225 230 235 240
 His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro Ser
 245 250 255
 Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys Gly
 260 265 270
 Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys Lys
 275 280 285
 Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro Asn
 290 295 300
 Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys Ser
 305 310 315 320
 Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser Pro
 325 330 335
 Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr Ser
 340 345 350
 Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn Pro

355	360	365
Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His Ala 370 375 380		
Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly Ala 385 390 395 400		
Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His Ile 405 410 415		
Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His Pro 420 425 430		
Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu Thr 435 440 445		
Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly Thr 450 455 460		
His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His Ile 465 470 475 480		
Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu Ile 485 490 495		
Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln Ser 500 505 510		
Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln Ile 515 520 525		
Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met Met 530 535 540		
Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr His 545 550 555 560		
Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln His 565 570 575		
Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser Gly 580 585 590		
His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser Pro 595 600 605		
Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser Asp 610 615 620		
Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg Gly 625 630 635 640		
Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val Tyr 645 650 655		

Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asp Ile Asp Glu Cys Asp Gln Gly Ser Pro Cys Glu His Asn Gly
1 5 10 15
Ile Cys Val Asn Thr Pro Gly Ser Tyr Arg Cys Asn Cys Ser Gln Gly
20 25 30
Phe Thr Gly Pro Arg Cys Glu Thr Asn Ile Asn Glu Cys Glu Ser His
35 40 45
Pro Cys Gln Asn Glu Gly Ser Cys Leu Asp Asp Pro Gly Thr Phe Arg
50 55 60
Cys Val Cys Met Pro Gly Phe Thr Gly Thr Gln Cys Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Asp Val Asp Glu Cys Ser Leu Gly Ala Asn Pro Cys Glu His Gly
1 5 10 15
Gly Arg Cys Thr Asn Thr Leu Gly Ser Phe Gln Cys Asn Cys Pro Gln
20 25 30
Gly Tyr Ala Gly Pro Arg Cys Glu Ile Asp Val Asn Glu Cys Leu Ser
35 40 45
Asn Pro Cys Gln Asn Asp Ser Thr Cys Leu Asp Gln Ile Gly Glu Phe
50 55 60
Gln Cys Ile Cys Met Pro Gly Tyr Glu Gly Leu Tyr Cys Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 654 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Pro Pro Gln Gly Glu Ile Glu Ala Asp Cys Met Asp Val Asn Val

1	5	10	15
Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly	20	25	30
Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Ser Ala	35	40	45
Asn Met Ile Ser Asp Phe Ile Gly Gln Gly Ala Gln Leu His Asn Gln	50	55	60
Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ala	65	70	75
Arg Ala Asp Ala Ala Lys Arg Leu Leu Glu Ser Ser Ala Asp Ala Asn	85	90	95
Val Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ala Ala	100	105	110
Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp	115	120	125
Leu Asp Ala Arg Met Phe Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala	130	135	140
Arg Leu Ala Val Glu Gly Met Val Glu Glu Leu Ile Asn Ala His Ala	145	150	155
Asp Val Asn Ala Val Asp Glu Phe Gly Lys Ser Ala Leu His Trp Ala	165	170	175
Ala Ala Val Asn Asn Val Asp Ala Ala Ala Val Leu Leu Lys Asn Ser	180	185	190
Ala Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Ser Leu Phe Leu	195	200	205
Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His	210	215	220
Tyr Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp	225	230	235
Ile Ala Gln Glu Arg Met His His Asp Ile Val His Leu Leu Asp Glu	245	250	255
Tyr Asn Leu Val Lys Ser Pro Thr Leu His Asn Gly Pro Leu Gly Ala	260	265	270
Thr Thr Leu Ser Pro Pro Ile Cys Ser Pro Asn Gly Tyr Met Gly Asn	275	280	285
Met Lys Pro Ser Val Gln Ser Lys Lys Ala Arg Lys Pro Ser Ile Lys	290	295	300
Gly Asn Gly Cys Lys Glu Ala Lys Glu Leu Lys Ala Arg Arg Lys Lys	305	310	315
Ser Gln Asp Gly Lys Thr Thr Leu Leu Asp Ser Gly Ser Ser Gly Val	325	330	335
Leu Ser Pro Val Asp Ser Leu Glu Ser Thr His Gly Tyr Leu Ser Asp	340	345	350
Val Ser Ser Pro Pro Leu Met Thr Ser Pro Phe Gln Gln Ser Pro Ser	355	360	365

Met Pro Leu Asn His Leu Thr Ser Met Pro Glu Ser Gln Leu Gly Met
 370 375 380

Asn His Ile Asn Met Ala Thr Lys Gln Glu Met Ala Ala Gly Ser Asn
 385 390 395 400

Arg Met Ala Phe Asp Ala Met Val Pro Arg Leu Thr His Leu Asn Ala
 405 410 415

Ser Ser Pro Asn Thr Ile Met Ser Asn Gly Ser Met His Phe Thr Val
 420 425 430

Gly Gly Ala Pro Thr Met Asn Ser Gln Cys Asp Trp Leu Ala Arg Leu
 435 440 445

Gln Asn Gly Met Val Gln Asn Gln Tyr Asp Pro Ile Arg Asn Gly Ile
 450 455 460

Gln Gln Gly Asn Ala Gln Gln Ala Gln Ala Leu Gln His Gly Leu Met
 465 470 475 480

Thr Ser Leu His Asn Gly Leu Pro Ala Thr Thr Leu Ser Gln Met Met
 485 490 495

Thr Tyr Gln Ala Met Pro Asn Thr Arg Leu Ala Asn Gln Pro His Leu
 500 505 510

Met Gln Ala Gln Gln Met Gln Gln Gln Gln Asn Leu Gln Leu His Gln
 515 520 525

Ser Met Gln Gln Gln His His Asn Ser Ser Thr Thr Ser Thr His Ile
 530 535 540

Asn Ser Pro Phe Cys Ser Ser Asp Ile Ser Gln Thr Asp Leu Gln Gln
 545 550 555 560

Met Ser Ser Asn Asn Ile His Ser Val Met Pro Gln Asp Thr Gln Ile
 565 570 575

Phe Ala Ala Ser Leu Pro Ser Asn Leu Thr Gln Ser Met Thr Thr Ala
 580 585 590

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Met Asp
 595 600 605

Asn Thr Pro Ser His Gln Leu Gln Val Pro Asp His Pro Phe Leu Thr
 610 615 620

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser
 625 630 635 640

Asn Met Ser Asp Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr
 645 650

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val
 1 5 10 15
 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly
 20 25 30
 Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala
 35 40 45
 Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
 50 55 60
 Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg
 65 70 75 80
 Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile
 85 90 95
 Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp
 100 105 110
 Ala Gln Gly Val Phe Gln Ile Leu Leu Arg Asn Arg Ala Thr Asp Leu
 115 120 125
 Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg
 130 135 140
 Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp
 145 150 155 160
 Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala
 165 170 175
 Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala
 180 185 190
 Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala
 195 200 205
 Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe
 210 215 220
 Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile
 225 230 235 240
 Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr
 245 250 255
 Asn Leu Val Arg Ser Pro Gln Leu His Gly Thr Ala Leu Gly Gly Thr
 260 265 270
 Pro Thr Leu Ser Pro Thr Leu Cys Ser Pro Asn Gly Tyr Leu Gly Asn
 275 280 285
 Leu Lys Ser Ala Thr Gln Gly Lys Lys Ala Arg Lys Pro Ser Thr Lys
 290 295 300
 Gly Leu Ala Cys Ser Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg
 305 310 315 320
 Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Ser Met
 325 330 335
 Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Gly Tyr Leu Ser Asp
 340 345 350
 Val Ala Ser Pro Pro Leu Pro Ser Pro Phe Gln Gln Ser Pro Ser Met

355	360	365
Pro Leu Ser His Leu Pro Gly Met Pro Asp Thr His Leu Gly Ile Ser 370 375 380		
His Leu Asn Val Ala Ala Lys Pro Glu Met Ala Ala Leu Ala Gly Gly 385 390 395 400		
Ser Arg Leu Ala Phe Glu Pro Pro Pro Pro Arg Leu Ser His Leu Pro 405 410 415		
Val Ala Ser Ser Ala Ser Thr Val Leu Ser Thr Asn Gly Thr Gly Ala 420 425 430		
Met Asn Phe Thr Val Gly Ala Pro Ala Ser Leu Asn Gly Gln Cys Glu 435 440 445		
Trp Leu Pro Arg Leu Gln Asn Gly Met Val Pro Ser Gln Tyr Asn Pro 450 455 460		
Leu Arg Pro Gly Val Thr Pro Gly Thr Leu Ser Thr Gln Ala Ala Gly 465 470 475 480		
Leu Gln His Gly Met Met Ser Pro Ile His Ser Ser Leu Ser Thr Asn 485 490 495		
Thr Leu Ser Pro Ile Ile Tyr Gln Gly Leu Pro Asn Thr Arg Leu Ala 500 505 510		
Thr Gln Pro His Leu Val Gln Thr Gln Gln Val Gln Pro Gln Asn Leu 515 520 525		
Gln Ile Gln Pro Gln Asn Leu Gln Pro Pro Ser Gln Pro His Leu Ser 530 535 540		
Val Ser Ser Ala Ala Asn Gly His Leu Gly Arg Ser Phe Leu Ser Gly 545 550 555 560		
Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly Pro Ser Ser Leu Pro 565 570 575		
Val His Thr Ile Leu Pro Gln Glu Ser Gln Ala Leu Pro Thr Ser Leu 580 585 590		
Pro Ser Ser Met Val Pro Pro Met Thr Thr Thr Gln Phe Leu Thr Pro 595 600 605		
Pro Ser Gln His Ser Tyr Ser Ser Ser Pro Val Asp Asn Thr Pro Ser 610 615 620		
His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr Pro Ser Pro Glu 625 630 635 640		
Ser Pro Asp Gln Trp Ser Ser Ser Ser Arg His Ser Asn Ile Ser Asp 645 650 655		
Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr 660 665		

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 681 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val
1           5           10           15
Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly
20           25           30
Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala
35           40           45
Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
50           55           60
Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg
65           70           75           80
Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile
85           90           95
Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp
100          105          110
Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp Leu
115          120          125
Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg
130          135          140
Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp
145          150          155          160
Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala
165          170          175
Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala
180          185          190
Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr Pro Leu Phe Leu Ala
195          200          205
Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe
210          215          220
Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile
225          230          235          240
Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr
245          250          255
Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala Pro Leu Gly Gly Thr
260          265          270
Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn Gly Tyr Leu Gly Ser
275          280          285
Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg Lys Pro Ser Ser Lys
290          295          300
Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg
305          310          315          320
Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Gly Met

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325	330	335
Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Gly Tyr Leu Ser Asp 340 345 350		
Val Ala Ser Pro Pro Leu Leu Pro Ser Pro Phe Gln Gln Ser Pro Ser 355 360 365		
Val Pro Leu Asn His Leu Pro Gly Met Pro Asp Thr His Leu Gly Ile 370 375 380		
Gly His Leu Asn Val Ala Ala Lys Pro Glu Met Ala Ala Leu Gly Gly 385 390 395 400		
Gly Gly Arg Leu Ala Phe Glu Thr Gly Pro Pro Arg Leu Ser His Leu 405 410 415		
Pro Val Ala Ser Gly Thr Ser Thr Val Leu Gly Ser Ser Ser Gly Gly 420 425 430		
Ala Leu Asn Phe Thr Val Gly Gly Ser Thr Ser Leu Asn Gly Gln Cys 435 440 445		
Glu Trp Leu Ser Arg Leu Gln Ser Gly Met Val Pro Asn Gln Tyr Asn 450 455 460		
Pro Leu Arg Gly Ser Val Ala Pro Gly Pro Leu Ser Thr Gln Ala Pro 465 470 475 480		
Ser Leu Gln His Gly Met Val Gly Pro Leu His Ser Ser Leu Ala Ala 485 490 495		
Ser Ala Leu Ser Gln Met Met Ser Tyr Gln Gly Leu Pro Ser Thr Arg 500 505 510		
Leu Ala Thr Gln Pro His Leu Val Gln Thr Gln Gln Val Gln Pro Gln 515 520 525		
Asn Leu Gln Met Gln Gln Gln Asn Leu Gln Pro Ala Asn Ile Gln Gln 530 535 540		
Gln Gln Ser Leu Gln Pro Pro Pro Pro Pro Gln Pro His Leu Gly 545 550 555 560		
Val Ser Ser Ala Ala Ser Gly His Leu Gly Arg Ser Phe Leu Ser Gly 565 570 575		
Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly Pro Ser Ser Leu Ala 580 585 590		
Val His Thr Ile Leu Pro Gln Glu Ser Pro Ala Leu Pro Thr Ser Leu 595 600 605		
Pro Ser Ser Leu Val Pro Pro Val Thr Ala Ala Gln Phe Leu Thr Pro 610 615 620		
Pro Ser Gln His Ser Tyr Ser Ser Pro Val Glu Asn Thr Pro Ser His 625 630 635 640		
Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr Pro Ser Pro Glu Ser 645 650 655		
Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Asn Val Ser Asp Trp 660 665 670		
Ser Glu Gly Val Ser Ser Pro Pro Thr 675 680		